FIGURE 1A

```
   1 CATTAANAGG TCCTGGCTGG GAGCTTTTTT TTGGGACCAG CACTCCATGT TCAAGGGCAA
  61 ACAGGGGCCA ATTAGGATCA ATCTTTTTTC TTTCTTTTTT TAAAAAAAAA AATTCTTCCC
 121 ACTTTGCACA CGGACAGTAG TACATACCAG TAGCTCTCTG CGAGGACGGT GATCACTAAT
 181 CATTTCTCCT GCTTCGTGGC AGATGAGTCC TACCAGACTT GTGAGGGTGC TGCTGGCTCT
 241 GGCCCTCATC TTGCCAGGGA AACTTTGTAC AAAAGGGACT GTTGGAAGGT CATCGATGGC
 301 CCGATGTAGC CTTCTCGGAG GTGACTTCAT CAACACCTTT GATGAGAGCA TGTACAGCTT
 361 TGCGGGAGAT TGCAGTTACC TCCTGGCTGG GGACTGCCAG GAACACTCCA TCTCACTTAT
 421 CGGGGGTTTC CAAAATGACA AAAGAGTGAG CCTCTCCGTG TATCTCGGAG AATTTTTCGA
 481 CATTCATTTG TTTGTCAATG GTACCATGCT GCAGGGGACC CAAAGCATCT CCATGCCCTA
 541 CGCCTCCAAT GGGCTGTATC TAGAGGCCGA GGCTGGCTAC TACAAGCTGT CCAGTGAGGC
 601 CTACGGCTTT GTGGCCAGAA TTGATGGCAA TGGCAACTTT CAAGTCCTGC TGTCAGACAG
 661 ATACTTCAAC AAGACCTGTG GGCTGTGTGG CAACTTTAAT ATCTTTGCTG AGGATGACTT
 721 CAAGACTCAA GAAGGGACGT TGACTTCGGA CCCCTATGAC TTTGCCAACT CCTGGGCCCT
 781 GAGCAGTGGG GAACAACGGT GCAAACGGGT GTCCCCTCCC AGCAGCCCAT GCAATGTCTC
 841 CTCTGATGAA GTGCAGCAGG TCCTGTGGGA GCAGTGCCAG CTCCTGAAGA GTGCCTCGGT
 901 GTTTGCCCGC TGCCACCCGC TGGTGGACCC TGAGCCTTTT GTCGCCCTGT GTGAAAGGAC
 961 TCTGTGCACC TGTGTCCAGG GGATGGAGTG CCCTTGTGCG GTCCTCCTGG AGTACGCCCG
1021 GGCCTGTGCC CAGCAGGGGA TTGTCTTGTA CGGCTGGACC GACCACAGCG TCTGCCGACC
1081 AGCATGCCCT GCTGGCATGG AGTACAAGGA GTGCGTGTCC CCTTGCACCA GAACTTGCCA
1141 GAGCCTTCAT GTCAAAGAAG TGTGTCAGGA GCAATGTGTA GATGGCTGCA GCTGCCCCGA
1201 GGGCCAGCTC CTGGATGAAG GCCACTGCGT GGGAAGTGCT GAGTGTTCCT GTGTGCATGC
1261 TGGGCAACGG TACCCTCCGG GCGCCTCCCT CTTACAGGAC TGCCACACCT GCATTTGCCG
1321 AAATAGCCTG TGGATCTGCA GCAATGAAGA ATGCCCAGGC GAGTGTCTGG TCACAGGACA
1381 GTCCCACTTC AAGAGCTTCG ACAACAGGTA CTTCACCTTC AGTGGGGTCT GCCACTACCT
1441 GCTGGCCCAG GACTGCCAGG ACCACACATT CTCTGTTGTC ATAGAGACTG TCCAGTGTGC
1501 CGATGACCTG GATGCTGTCT GCACCCGTCC GGTCACCGTC CGCCTGCCTG GACATCACAA
1561 CAGCCTTGTG AAGCTGAAGA ATGGGGGAGG AGTCTCCATG GATGGCCAGG ATATCCAGAT
1621 TCCTCTCCTG CAAGGTGACC TCCGCATCCA GCACACCGTG ATGGCCTCCG TGCGCCTCAG
1681 CTACGGGGAG GACCTGCAGA TGGATTCGGA CGTCCGGGGC AGGCTACTGG TGACGCTGTA
1741 CCCCGCCTAC GCGGGGAAGA CGTGCGGCCG TGGCGGGAAC TACAACGGCA ACCGGGGGGA
1801 CGACTTCGTG ACGCCCGCAG GCCTGGCGGA GCCCCTGGTG GAGGACTTCG GGAACGCCTG
1861 GAAGCTGCTC GGGGCCTGCG AGAACCTGCA GAAGCAGCAC CGCGATCCCT GCAGCCTCAA
1921 CCCGCGCCAG GCCAGGTTTG CGGAGGAGGC GTGCGCGCTG CTGACGTCCT CGAAGTTCGA
1981 GCCCTGCCAC CGAGCGGTGG GTCCTCAGCC CTACGTGCAG AACTGCCTCT ACGACGTCTG
2041 CTCCTGCTCC GACGGCAGAG ACTGTCTTTG CAGCGCCGTG GCCAACTACG CCGCAGCCGT
2101 GGCCCGGAGG GGCGTGCACA TCGCGTGGCG GGAGCCGGGC TTCTGTGCGC TGAGCTGCCC
2161 CCAGGGCCAG GTGTACCTGC AGTGTGGGAC CCCCTGCAAC ATGACCTGTC TCTCCCTCTC
2221 TTACCCGGAG GAGGACTGCA ATGAGGTCTG CTTGGAAAGC TGCTTCTCCC CCCCAGGGCT
2281 GTACCTGGAT GAGAGGGGAG ATTGTGTGCC CAAGGCTCAG TGTCCCTGTT ACTATGATGG
2341 TGAGATCTTT CAGCCCGAAG ACATCTTCTC AGACCATCAC ACCATGTGCT ACTGTGAGGA
2401 TGGCTTCATG CACTGTACCA CAAGTGGAGG CCTGGGAAGC CTGCTGCCCA ACCCGGTGCT
2461 CAGCAGCCCC CGGTGTCACC GCAGCAAAAG GAGCCTGTCC TGTCGGCCCC CCATGGTCAA
2521 GTTGGTGTGT CCCGCTGATA ACCCGAGGGC TGAAGGACTG GAGTGTGCCA AAACCTGCCA
2581 GAACTATGAC CTGCAGTGCA TGAGCACAGG CTGTGTCTCC GGCTGCCTCT GCCCGCAGGG
2641 CATGGTCCGG CATGAAAACA GGTGTGTGGC GCTGGAAAGA TGTCCCTGCT TCCACCAAGG
2701 CCAAGAGTAC GCCCCAGGAG AAACCGTGAA AATTGACTGC AACACTTGTG TCTGTCGGGA
     TGGAAGTG   TTTGCACA   CCATGTGT   TTATGGCAC   TTCTGCCT   TGGCATGC
     GCACTACCTC ACCTTCGACC GACTCAAGTA CCTGTTCCT GGGGAGTGCC AGTATGTTC
     GGTGCAGGAT TACTGCGGCA GTAACCCTGG GACCTTACGG ATCCTGGTGG GGAACGAGGG
2941 GTGCAGCTAC CCCTCAGTGA AATGCAAGAA GCGGGTCATC ATCCTGGTGG AAGGAGGAGA
3001 GATTGAACTG TTTGATGGGG AGGTGAATGT GAAGAAACCC ATGAAGGATG AGACTCACTT
3061 TGAGGTGGTA GAGTCTGGTC AGTACGTCAT TCTGCTGCTG GGCAAGGCAC TCTCTGTGGT
3121 CTGGGACCAC CGCCTGAGCCA TCTCTGTGAC CCTGAAGCGG ACATACCAGG AGCAGGTGTG
```

FIGURE 1B

```
3181 TGGCCTGTGT GGGAATTTTG ATGGCATCCA GAACAATGAT TTCACCAGCA GCAGCCTCCA
3241 AATAGAAGAA GACCCTGTGG ACTTTGGGAA TTCCTGGAAA GTGAACCCGC AGTGTGCCGA
3301 CACCAAGAAA GTACCACTGG ACTCATCCCC TGCCGTCTGC CACAACAACA TCATGAAGCA
3361 GACGATGGTG GATTCCTCCT GCAGGATCCT CACCAGTGAT ATTTTCCAGG ACTGCAACAG
3421 GCTGGTGGAC CCTGAGCCAT TCCTGGACAT TTGCATCTAC GACACTTGCT CCTGTGAGTC
3481 CATTGGGGAC TGCACCTGCT TCTGTGACAC CATTGCTGCT TACGCCCACG TCTGTGCCCA
3541 GCATGGCAAG GTGGTAGCCT GGAGGACAGC CACATTCTGT CCCCAGAATT GCGAGGAGCG
3601 GAATCTCCAC GAGAATGGGT ATGAGTGTGA GTGGCGCTAT AACAGCTGTG CCCCTGCCTG
3661 TCCCATCACG TGCCAGCACC CCGAGCCACT GGCATGCCCT GTACAGTGTG TTGAAGGTTG
3721 CCATGCGCAC TGCCCTCCAG GGAAAATCCT GGATGAGCTT TTGCAGACCT GCATCGACCC
3781 TGAAGACTGT CCTGTGTGTG AGGTGGCTGG TCGTCGCTTG GCCCCAGGAA AGAAAATCAT
3841 CTTGAACCCC AGTGACCCTG AGCACTGCCA AATTTGTAAT TGTGATGGTG TCAACTTCAC
3901 CTGTAAGGCC TGCAGAGAAC CCGGAAGTGT TGTGGTGCCC CCACAGATG GCCCCATTGG
3961 CTCTACCACC TCGTATGTGG AGGACACGTC GGAGCCGCCC CTCCATGACT TCCACTGCAG
4021 CAGGCTTCTG GACCTGGTTT TCCTGCTGGA TGGCTCCTCC AAGCTGTCTG AGGACGAGTT
4081 TGAAGTGCTG AAGGTCTTTG TGGTGGGTAT GATGGAGCAT CTGCACATCT CCCAGAAGCG
4141 GATCCGCGTG GCTGTGGTGG AGTACCACGA CGGCTCCCAC GCCTACATCG AGCTCAAGGA
4201 CCGGAAGCGA CCCTCAGAGC TGCGGCGCAT CACCAGCCAG GTGAAGTACG CGGGCAGCGA
4261 GGTGGCCTCC ACCAGTGAGG TCTTAAAGTA CACGCTGTTC CAGATCTTTG GCAAGATCGA
4321 CCGCCCGGAA GCGTCTCGCA TTGCCCTGCT CCTGATGGCC AGCCAGGAGC CCTCAAGGCT
4381 GGCCCGGAAT TTGGTCCGCT ATGTGCAGGG CCTGAAGAAG AAGAAAGTCA TTGTCATCCC
4441 TGTGGGCATC GGGCCCCACG CCAGCCTTAA GCAGATCCAC CTCATAGAGA AGCAGGCCCC
4501 TGAGAACAAG GCCTTTGTGT TCAGTGGTGT GGATGAGTTG GAGCAGCGAA GGGATGAGAT
4561 TATCAACTAC CTCTGTGACC TTGCCCCCGA AGCACCTGCC CCTACTCAGC ACCCCCCAAT
4621 GGCCCAGGTC ACGGTGGGTT CGGAGCTGTT GGGGGTTTCA TCTCCAGGAC CCAAAAGGAA
4681 CTCCATGGTC CTGGATGTGG TGTTTGTCCT GGAAGGGTCA GACAAAATTG GTGAGGCCAA
4741 CTTTAACAAA AGCAGGGAGT TCATGGAGGA GGTGATTCAG CGGATGGACG TGGGCCAGGA
4801 CAGGATCCAC GTCACAGTGC TGCAGTACTC GTACATGGTG ACCGTGGAGT ACACCTTCAG
4861 CGAGGCGCAG TCCAAGGGCG AGGTCCTACA GCAGGTGCGG GATATCCGAT ACCGGGGTGG
4921 CAACAGGACC AACACTGGAC TGGCCCTGCA ATACCTGTCC GAACACAGCT TCTCGGTCAG
4981 CCAGGGGGAC CGGGAGCAGG TACCTAACCT GGTCTACATG GTCACAGGAA ACCCCGCTTC
5041 TGATGAGATC AAGCGGATGC CTGGAGACAT CCAGGTGGTG CCCATCGGGG TGGGTCCACA
5101 TGCCAATGTG CAGGAGCTGG AGAAGATTGG CTGGCCCAAT GCCCCCATCC TCATCCATGA
5161 CTTTGAGATG CTCCCTCGAG AGGCTCCTGA TCTGGTGCTA CAGAGGTGCT GCTCTGGAGA
5221 GGGGCTGCAG ATCCCCACCC TCTCCCCCAC CCCAGATTGC AGCCAGCCCC TGGATGTGGT
5281 CCTCCTCCTG GATGGCTCTT CCAGCATTCC AGCTTCTTAC TTTGATGAAA TGAAGAGCTT
5341 CACCAAGGCT TTTATTTCAA GAGCTAATAT AGGGCCCCGG CTCACTCAAG TGTCGGTGCT
5401 GCAATATGGA AGCATCACCA CTATCGATGT GCCTTGGAAT GTAGCCTATG AGAAAGTCCA
5461 TTTACTGAGC CTTGTGGACC TCATGCAGCA GGAGGGAGGC CCCAGCGAAA TTGGGGATGC
5521 TTTGAGCTTT GCCGTGCGAT ATGTCACCTC AGAAGTCCAT GGTGCCAGGC CCGGAGCCTC
5581 GAAAGCGGTG GTTATCCTAG TCACAGATGT CTCCGTGGAT TCAGTGGATG CTGCAGCCGA
5641 GGCCGCCAGA TCCAACCGAG TGACAGTGTT CCCCATTGGA ATCGGGGATC GGTACAGTGA
5701 GGCCCAGCTG AGCAGCTTGG CAGGCCCAAA GGCTGGCTCC AATATGGTAA GGCTCCAGCG
5761 AATTGAAGAC CTCCCCACCG TGGCCACCCT GGGAAATTCC TTCTTCCACA AGCTGTGCTC
5821 TGGGTTTGAT AGAGTTTGCG TGGATGAGGA·TGGGAATGAG AAGAGGCCCG GGGATGTCTG
5881 GACCTTGCCA GACCAGTGCC ACACAGTGAC TTGCCTGCCA GATGGCCAGA CCTTGCTGAA
5941 GAGTCATCGG GTCAACTGTG ACCGGGGGCC AAGGCCTTCG TGCCCCAATG GCCAGCCCCC
     TTCAGGTT  AGGAGACT  ATGGTGCC       ACGACTT  TCTGTGTT   AATCCCT
...  TCTACCCGC CACATCGTGA ACTTTGATG· ·CAGAATTT· ·AGCTGACTG GCAGCTGTT
...  ·CTATGTCCTA TTTCAAAACA AGGAGCAGCA CCTGGAGGT· ATTCTCCAGA ATGGTGCT·
6181 CAGCCCTGGC GCGAAGGAGA CCTGCATGAA ATCCATTGAG GTGAAGCATG ACGGCCTCTC
6241 AGTTGAGCTC CACAGTGACA TGCAGATGAC AGTGAATGGG AGACTAGTCT CCATCCCATA
6301 TGTGGGTGGA GACATGGAAG TCAATGTTTA TGGGACCATC ATGTATGAGG TCAGATTCAA
6361 CCATCTTGGC CACATCTTCA CATTCACCCC CCAAAACAAT GAGTTCCAGC TGCAGCTCAG
```

FIGURE 1C

```
6421 CCCCAGGACC TTTGCTTCGA AGACATATGG TCTCTGTGGG ATCTGTGATG AGAACGGAGC
6481 CAATGACTTC ATTCTGAGGG ATGGGACAGT CACCACAGAC TGGAAGGCAC TCATCCAGGA
6541 ATGGACCGTA CAGCAGCTTG GGAAGACATC CCAGCCTGTC CATGAGGAGC AGTGTCCTGT
6601 CTCCGAATTC TTCCACTGCC AGGTCCTCCT CTCAGAATTG TTTGCCGAGT GCCACAAGGT
6661 CCTCGCTCCA·GCCACCTTTT ATGCCATGTG CCAGCCCGAC AGTTGCCACC CGAAGAAAGT
6721 GTGTGAGGCG ATTGCCTTGT ATGCCCACCT CTGTCGGACC AAAGGGGTCT GTGTGGACTG
6781 GAGGAGGGGC AATTTCTGTG CTATGTCATG TCCACCATCC CTGGTGTACA ACCACTGTGA
6841 GCATGGCTGC CCTCGGCTCT GTGAAGGCAA TACAAGCTCC TGTGGGGACC AACCCTCGGA
6901 AGGCTGCTTC TGCCCCCCAA ACCAAGTCAT GCTGGAAGGT AGCTGTGTCC CCGAGGAGGC
6961 CTGTACCCAG TGCATCAGCG AGGATGGAGT CCGGCACCAG TTCCTGGAAA CCTGGGTCCC
7021 AGCCCACCAG CCTTGCCAGA TCTGCACGTG CCTCAGTGGG CGGAAGGTCA ACTGTACGTT
7081 GCAGCCCTGC CCCACAGCCA AAGCTCCCAC CTGTGGCCCG TGTGAAGTGG CCCGCCTCCG
7141 CCAGAACGCA GTGCAGTGCT GCCCGGAGTA CGAGTGTGTG TGTGACCTGG TGAGCTGTGA
7201 CCTGCCCCCG GTGCCTCCCT GCGAAGATGG CCTCCAGATG ACCCTGACCA ATCCTGGCGA
7261 GTGCAGACCC AACTTCACCT GTGCCTGCAG GAAGGATGAA TGCAGACGGG AGTCCCCGCC
7321 CTCTTGTCCC CCGCACCGGA CGCCGGCCCT TCGGAAGACT CAGTGCTGTG ATGAGTATGA
7381 GTGTGCATGC AACTGTGTCA ACTCCACGGT GAGCTGCCCG CTTGGGTACC TGGCCTCGGC
7441 TGTCACCAAC GACTGTGGCT GCACCACAAC AACCTGCTTC CCTGACAAGG TGTGTGTCCA
7501 CCGAGGCACC ATCTACCCTG TGGGCCAGTT CTGGGAGGAG GCCTGTGACG TGTGCACCTG
7561 CACGGACTTG GAGGACTCTG TGATGGGCCT GCGTGTGGCC CAGTGCTCCC AGAAGCCCTG
7621 TGAGGACAAC TGCCTGTCAG GCTTCACTTA TGTCCTTCAT GAAGGCGAGT GCTGTGGAAG
7681 GTGTCTGCCA TCTGCCTGTG AGGTGGTCAC TGGTTCACCA CGGGGCGACG CCCAGTCTCA
7741 CTGGAAGAAT GTTGGCTCTC ACTGGGCCTC CCCTGACAAC CCCTGCCTCA TCAATGAGTG
7801 TGTCCGAGTG AAGGAAGAGG TCTTTGTGCA ACAGAGGAAT GTCTCCTGCC CCCAGCTGAA
7861 TGTCCCCACC TGCCCCACGG GCTTCCAGCT GAGCTGTAAG ACCTCAGAGT GTTGTCCCAC
7921 CTGTCACTGC GAGCCCCTGG AGGCCTGCTT GCTCAATGGT ACCATCATTG GGCCGGGGAA
7981 AAGTCTGATG ATTGATGTGT GTACAACCTG CCGCTGCACC GTGCCGGTGG GAGTCATCTC
8041 TGGATTCAAG CTGGAGGGCA GGAAGACCAC CTGTGAGGCA TGCCCCCTGG GTTATAAGGA
8101 AGAGAAGAAC CAAGGTGAAT GCTGTGGGAG ATGTCTGCCT ATAGCTTGCA CCATTCAGCT
8161 AAGAGGAGGA CAGATCATGA CACTGAAGCG TGATGAGACT ATCCAGGATG GCTGTGACAG
8221 TCACTTCTGC AAGGTCAATG AAGAGGAGA GTACATCTGG GAGAAGAGAG TCACGGGTTG
8281 CCCACCTTTC GATGAACACA AGTGTCTGGC TGAGGGAGGA AAAATCATGA AAATTCCAGG
8341 CACCTGCTGT GACACATGTG AGGAGCCAGA ATGCAAGGAT ATCATTGCCA AGCTGCAGCG
8401 TGTCAAAGTG GGAGACTGTA AGTCTGAAGA GGAAGTGGAC ATTCATTACT GTGAGGGTAA
8461 ATGTGCCAGC AAAGCCGTGT ACTCCATCCA CATGGAGGAT GTGCAGGACC AGTGCTCCTG
8521 CTGCTCGCCC ACCCAGACGG AGCCCATGCA GGTGGCCCTG CGCTGCACCA ATGGCTCCCT
8581 CATCTACCAT GAGATCCTCA ATGCCATCGA ATGCAGGTGT TCCCCCAGGA AGTGCAGCAA
8641 GTGAGGCCAC TGCCTGGATG CTACTGTCGC CTGCCTTACC CGACCTCACT GGACTGGCCA
8701 GAGTGCTGCT CAGTCCTCCT CAGTCCTCCT CCTGCTCTGC TCTTGTGCTT CCTGATCCCA
8761 CAATAAAGGT CAATCTTTCA CCTTGAAAAA AAAAAAAAA AA
```

```
Human    MIPARFAGVLLALALILPGTLCAEGTRGRSSTARCSLFGSDFVNTFDGSMYSFAGYCSYL    60
Dog      -S-T-LVR-----------K--TK--V----M-----L-G--I----E-------D----

Human    LAGGCQFRSFSIIGDFQNGKRVSLSVYLGEFFDIHLFVNGTVTQGDQRVSMPYASKGLYL   120
Dog      ---D--EH-I-L--G---D---------------------ML--T-SI------N----

Human    ETEAGYYKLSGEAYGFVARIDGSGNFQVLLSDRYFNTICGLCGNFNIFAEDDFMTQEGTL   180
Dog      -A--------S----------N----------------------------K------

Human    TSDPYDFANSWALSSGEQWCERASPPSSSCNISSGEMQKGLWEQCQLLKSTSVFARCHPL   240
Dog      -----------------R-K-V-----P--V--D-V-QV----------A------

Human    VDPEPFVALCEKTLCECAGGLECACPALLEYARTCAQEGMVLYGWTDHSACSPVCPAGME   300
Dog      ----------R---T-VQ-M--P-AV------A---Q-I---------V-R-A-----

Human    YRQCVSPCARTCQSLHINZMCQERCVDGCSCPEGQLLDEGLCVESTECPCVHSGKRYPPG   360
Dog      -KE-----T-------VK-V---Q---------------H--G-A--S---A-Q-----

Human    TSLSRDCNTCICPNSQWICSNEECPGECLVTGQSHFKSFDNRYFTFSGICQYLLARDCQD   420
Dog      A--LQ--H--------L-----------------------------V-H---Q----

Human    HSFSIVIETVQCADDRDAVCTRSVTVRLPGLENSLVKLYHGAGVANDGQDVQLPLLKGDL   480
Dog      -T--V------------L---------------H--------N-G--S-----I-I---Q--

Human    RIQHTVTASVRLSYGEDLQMDWDGRGRLLVKLSPVYAGKTCGLCGNYNGNQGDDFLTPSG   540
Dog      ------M------------S-V----T-Y-A-------RG------R----V--A-

Human    LAEPRVEDFGNAWKLHGDCQDLQKQHSDPCALNPPMTRFSEEACAVLTSPTFEACHRAVS   600
Dog      ----L----------L-A-EN-----R---S----QA--A-----L---SK--P-----G

Human    PLPYLRNCRYDVCSCSDGRECLCGALASYAAACAGRGVRVAWREPGRCELNCPKGQVYLQ   660
Dog      -Q--VQ--L----------D---S-V-N----V-R---HI------F-A-S--Q-----

Human    CGTPCNLTCRSLSYPDEECHEACLEGCFCPPGLYNDERGDCVPKAQCPCYYDGEIFQPED   720
Dog      ------M--L-----E-D---V---S--S-----L-..
```
(box around "RGD")
```
Human    IFSDHHTMCYCEDGFMHCTMSGVPGSLLPDAVLSSPLSHRSKRSLSCRPPMVKLVCPADN   780
Dog      --------------------T--GL-----NP-----RC-------------------

Human    LRAEGLECTKTCQNYDLECMSHGCVSGCLCPPGMVRHENRCVALERCPCFHQGKEYAPGE   840
Dog      P-------A--------Q---T---------Q--------------------Q----?

Human    TVKIGCNTCVCRDRKWNCTDHVCDATCSTIGMAHYLTFDGLKYLFPGECQYVLVQDYCGS   900
Dog      ----D-----------T----------A--------------------------

Human    NPGTFRILVGNKGCSHPSVKCKKRVTILVEGGEIELFDGEVNVKRPMKDETHFEVVESGR   960
Dog      ----L------E---Y-------------------------K-------------Q

Human    IGNSWKVSSQCADTRKVFLDSSFATCHRNIMKQTMVDSSCRILTSDVFQDCNKLVDPEPY  1080
Dog      -------NP-----K---------V---------------I-----R------F
```

FIGURE 2A

```
Human   LDVCIYDTCSCESIGDCACFCDTIAAYAHVCAQHGKVVTWRTATLCPQSCEERNLRENGY
Dog     --I---------------T---------------------------A-----F---N-----H----   1140

Human   ECEWRYNSCAPACQVTCQHPEPLACPVQCVEGCHAHCPPGKILDELLQTCVDPEDCPVCE
Dog     -------------PI----------------------------------------I---------   1200

Human   VAGRRFASGKKVTLNPSDPEHCQICHCDVVNLTCEACQEPGGLVVPPTDAPVSPTTLYVE
Dog     -----L-P---II------------N--G--F--K--R----SV------G-IGS--S---   1260

Human   DISEPPLHDFYCSRLLDLVFLLDGSSRLSEAEFEVLKAFVVDMMERLRISQKHVRVAVVE
Dog     -T--------H--------------K---D------V---G---H-H----RI------   1320

Human   YHDGSHAYIGLKDRKRPSELRRIASQVKYAGSQVASTEVLKYTLFQIFSKIDRPEASRI
Dog     ---------E=-----------T--------E-----------------J---------   1380

Human   ALLLMASQEPQRMSRNFVRYVQGLKKKKVIVIPVGIGPHANLKQIRLIEKQAPENKAFVL
Dog     ----------S-LA--L------------------------------S----H----------F   1440

Human   SSVDELEQQRDEIVSYLCDLAPEAPPPTLPPEMAQVTVGPGLLGVSTLGPKRNSMVLDVA
Dog     -G------R----IN----------A--QH-P-------SE-----SP----------V   1500

Human   FVLEGSDKIGEADFNRSKEFMEEVIQRMDVGQDSIHVTVLQYSYMVTVEYPFSEAQSKGD
Dog     ------------N--K-R-------------------R-----------------T--------E   1560

Human   ILQRVREIRYQGGNRTNTGLALRYLSDHSFLVSQGDREQAPNLVYMVTGNPASDEIKRLP
Dog     V--Q--D---R----------Q---E---S--------V----------------M-   1620

Human   GDIQVVPIGVGPNANVQELERIGWPNAPILIQDFETLPREAPDLVLQRCCSGEGLQIPTL
Dog     ------------H-------K-----------H---M---------------------   1680

Human   SPAPDCSQPLDVILLLDGSSSFPASYFDEMKSFAKAFISKANIGPRLTQVSVLQYGSITT
Dog     --T---------V---------I------------T-----R-----------------   1740

Human   IDVPWNVVPEKAHLLSLVDVMQREGGPSQIGDALGFAVRYLTSEMHGARPGASKAVVILV
Dog     -------AY--V-------L--Q-----E-----S-----V---V--------------   1800

Human   TDVSVDSVDAAADAARSNRVTVFPIGIGDRYDAAQLRILAGPAGDSNVVKLQRIEDLPTM
Dog     -----------E------------------SE---SS----KAG--M-R----------V   1860

Human   VTLGNSFLHKLCSGFVRICMDEDGNEKRPGDVWTLPDQCHTVTCQPDGQTLLKTHRVNCD
Dog     A------F---------D-V-V-------------------------L--------S----   1920

Human   RGLRPSCPNSQSPVKVEETCGCRWTCPCVCTGSSTRHIVTFDGQNFKLTGSCSYVLFQNK
Dog     --P-------G-P-LR-------------------H----------------------   1980

Human   EQDLEVILHNGACSPGARQGCMKSIEVKHSALSVELHSDMEVTVNGRLVSVPYVGGNMEV
Dog     --------Q--------KET---------DG---------QM--------I-----D---   2040

Human   NVYGAIMHEVRFNHLGHIFTFT...

...LQHTVGRFGQTCQPILEEQQLVTDSSWQQLLLPLFKEGHKNLAPATFI
--A-I-------CD-K-S--VH----P-SEFF------SE--------------   210.
```

FIGURE 2B

```
Human   AICQQDSCHQEQVCEVIASYAHLCRTNGVCVDWRTPDFCAMSCPPSLVYNHCEHGCPRHC   2220
Dog     -M--P----PKK---A--L--------K-------RAN--------------------L-

Human   DGNVSSCGDHPSEGCFCPPDKVMLEGSCVPEEACTQCIGEDGVQHQFLEAWVPDHQPCQI   2280
Dog     E--T-----Q---------NQ-----------------S----R-----T---A------

Human   CTCLSGRKVNCTTQPCPTAKAPTCGLCEVARLRQNADQCCPEYECVCDPVSCDLPPVPHC   2340
Dog     ------------L------------P-----------V-----------L---------P-

Human   ERGLQPTLTNPGECRPNFTCACRKEECKRVSPPSCPPHRLPTLRKTQCCDEYECACNCVN   2400
Dog     -D---M------------------D--R-E---------T-A------------------

Human   STVSCPLGYLASTATNDCGCTTTTCLPDKVCVHRSTIYPVGQFWEEGCDVCTCTDMEDAV   2460
Dog     ------------AV-----------F--------G-----------A---------L--S-

Human   MGLRVAQCSQKPCEDSCRSGFTYVLHEGECCGRCLPSACEVVTGSFRGDSQSSWKSVGSQ   2520
Dog     --------------N-L-----------------------------A--H--N---H

Human   WASPENPCLINECVRVKEEVFIQQRNVSCPQLEVPVCPSGFQLSCKTSACCPSCRCEFNE   2580
Dog     ----D----------------V----------N--T--T---------E---T-H--PL-

Human   ACMLNGTVIGPGKTWMIDVCTTCRCMVQVGVISGFKLECRKTTCNPCPLGYKEENTGEC   2640
Dog     --L----I-----SL----------T-P----------G-----EA--------K-Q---

Human   CGRCLPTACTIQLRGGQIMTLKRDETLQDGCDTHFCKVNERGEYFWEKRVTGCPPFDEHK   2700
Dog     ------I------------------I-----S---------I---------------

Human   CLAEGGKIMKIPGTCCDTCEEPECNDITARLQYVKVGSCKSEVEVDIHYCQGKCASKANY   2760
Dog     ------------------------K--I-K--R----D----E-------E-------V-

Human   SIDINDVQDQCSCCSPTRTEPMQVALHCTNGSVVYHEVLNANECKCSPRKCSK         2813
Dog     --HME-----------Q--------R-----LI---I---I--R--------
```

FIGURE 2C

FIG. 3.

```
exon 4        AAATGACAAAAGAGTGAGCCGGTC*
AGGGGTTTCCAAAATGACAAAAGAGTGAGCCTCTCCGTGTATCTCGGAGAATTTTTCGA
   G  G  F  Q  N  D  K  R  V  S  L  S  V  Y  L  G  E  F  F  D

CATTCATTTGTTTGTCAATGGTACCATGCTGCAGGGGACCCAAAGGTAAGTCAGAAGCCC
   I  H  L  F  V  N  G  T  M  L  Q  G  T  Q  R

GAATGTTCAGGTTAATATGGACCCTGGGGATCACTTTGCAACCCCCTTGTTTTTTCAGAT

GAGGGAGCCGGGGCCCAGAGACAGGAAGTAAATGTGCCCAGGGAAAGTGAGTGGCAGGAC

TGGGTGAAAGCCCCATATCCCGACTCCTGGTCAAGGAGACTTTGCACCAAGGTCCCAGCC
                3'-GGGCTGGCGACCAGTTCCTCTGAA-5'

CTGGAGCATGGGGGTTGGGGTTGGAAGGTGGAGGGACATGGAGGAAATGCATGAGAAGCAC

                       exon 5
GCTTCCTGAGCTCCTCCTTGTCCCACCAGCATCTCCATGCCCTACGCCTCCAATGGGC
                       I  S  M  P  Y  A  S  N  G
```

FIGURE 4

FIG. 5.

Normal Allele

Exon 43   Intron 43   Exon 44

                                    •
AGGACAACTGCCTGCCTGTC**G**gtgagtgggg ... GGCTTCACTTAT
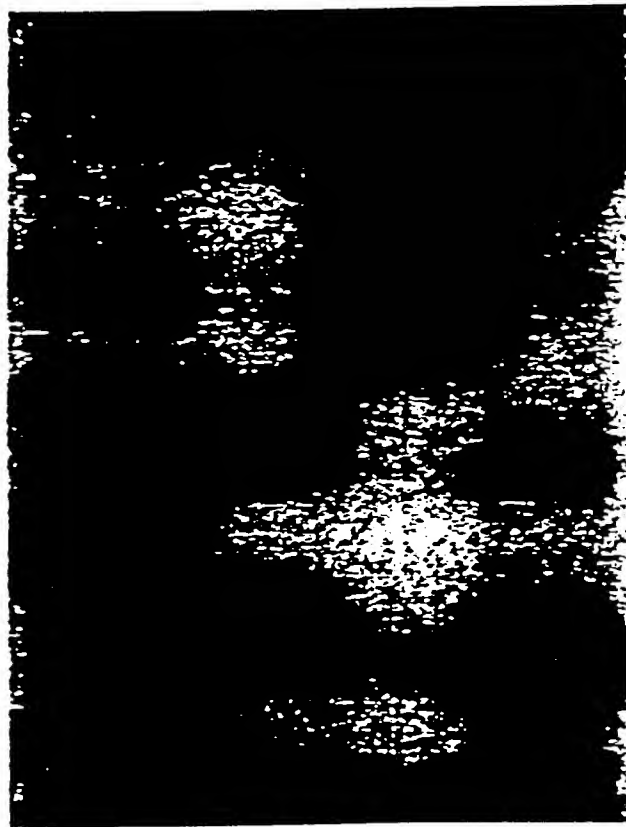 | | | | | | |
                             AGGTRAGT   Donor Consensus

Mutant Allele

                                    •
AGGACAACTGCCTGCC**T**gtcagtgagtgggg ... GGCTTCACTTAT
                             | | | | |
                       AGGTRAGT   Donor Consensus

Figure 6

Figure 7

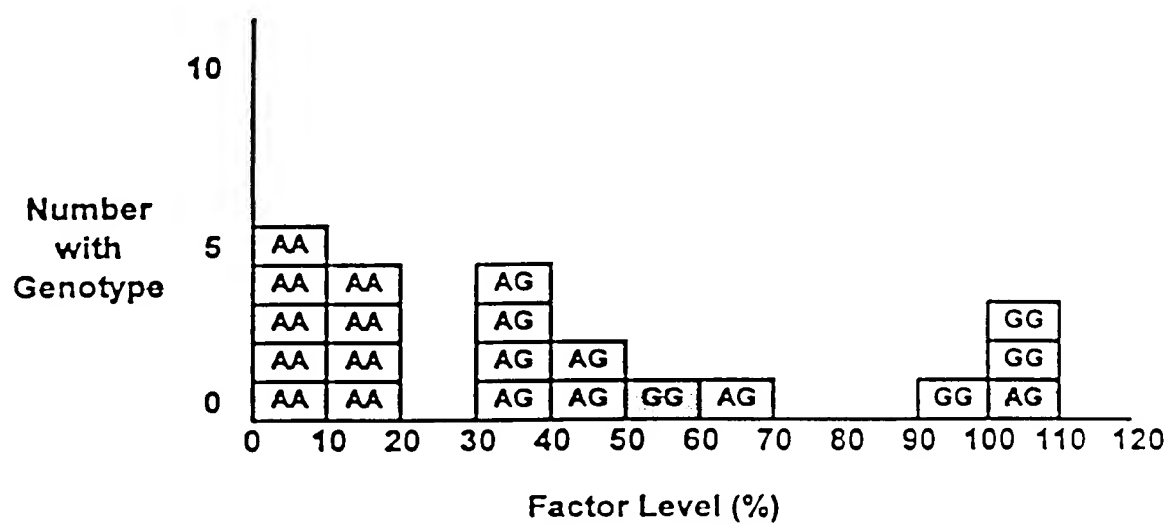C T A G
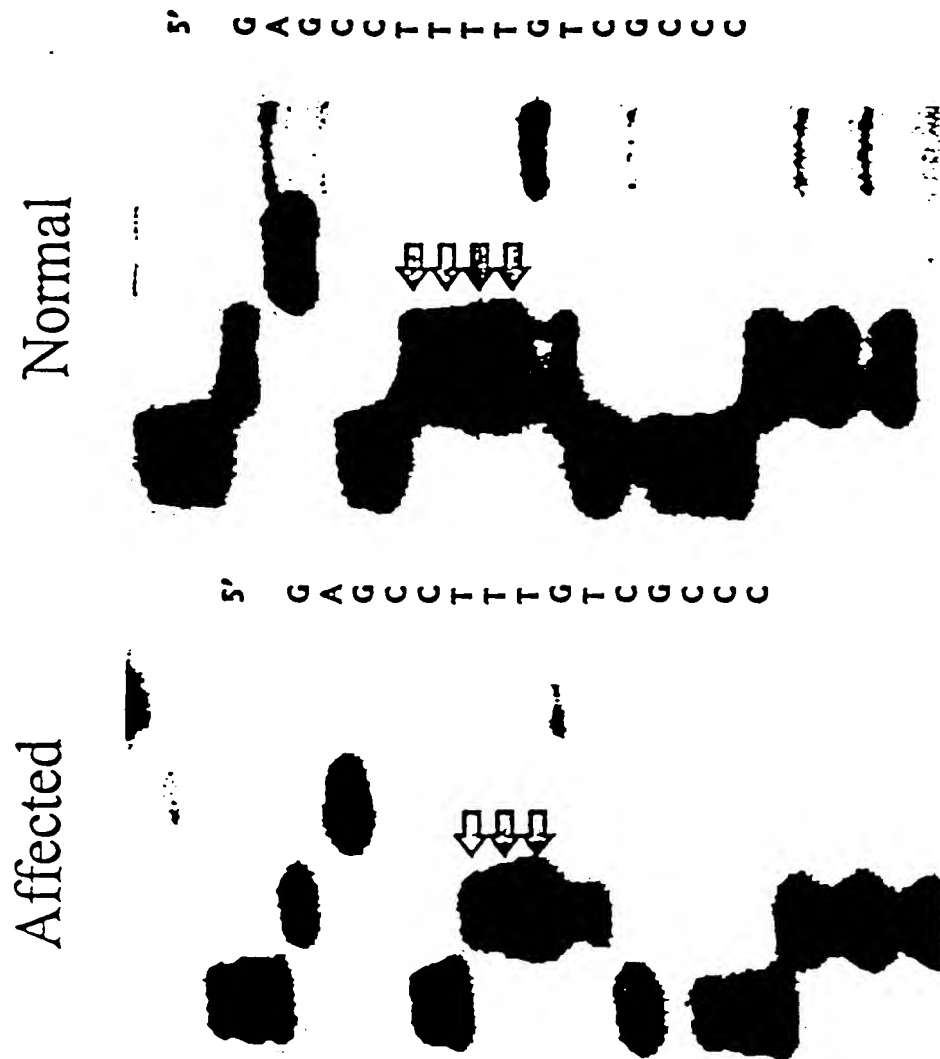
5'

A
G
G
A
C
A
A
C
T
G
C
C
T
G
G
C
T
T

3'

G
T
C
A
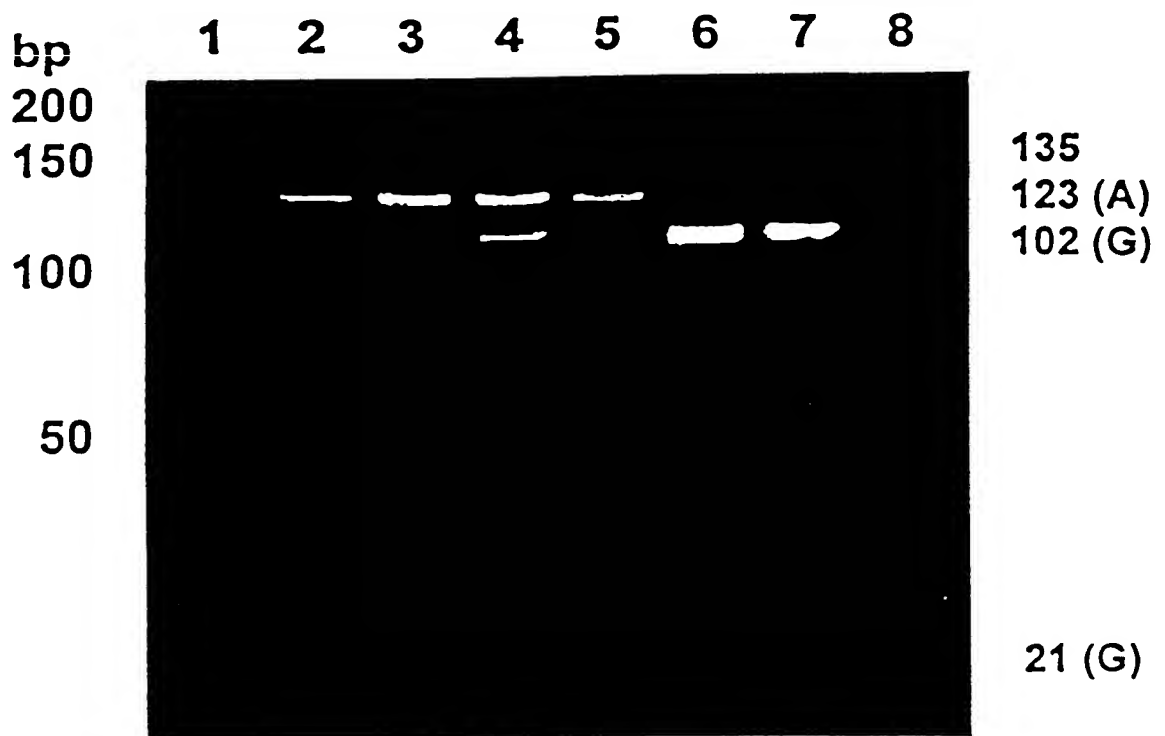
Figure 8

Figure 9

Figure 10

Exon 7

```
        V   L   W   E   Q   C   Q   L   L   K   S   A   S   V   F   A   R   C   H   P   L   V
        GTCCTGTGGGAGCAGTGCCAGCTCCTGAAGAGTGCCTCGGTGTTGCCCGCTGCCACCCGCTGGTG
        TCCTGTGGGAGCAGTGCCAG
DVWFEX7D   GCNNNNNNNGC  Mwo I

        D   P   E   P   F   V   A   L   C   E   R   T   L   C   T   C   V   C   G   M   E   C
        GACCCTGAGCCTTTTGTCGCCCTGTGTGAAAGGACTCTGTGCACCTGTGTCCAGGGGATGGAGTGC
               GCNNNNN-NNNGC   Mwo I
                    Δ735

        P   C   A   V   L   L   E   Y   A   R   A   C   A   Q   Q   G   I   V   L   Y   G   W
        CCTTGTGCGGTCCTCCTGGAGTACGCCCGGGCCTGTGCCCAGCAGGGAATTGT?GCTGTACGGCTGG
                                                               ATGCCGACC

        T   D   H   S   V   C   R
        ACCGACCACAGCGTCTGCCG
        TGGCTGGTG-5'
DVWFEX7U
```
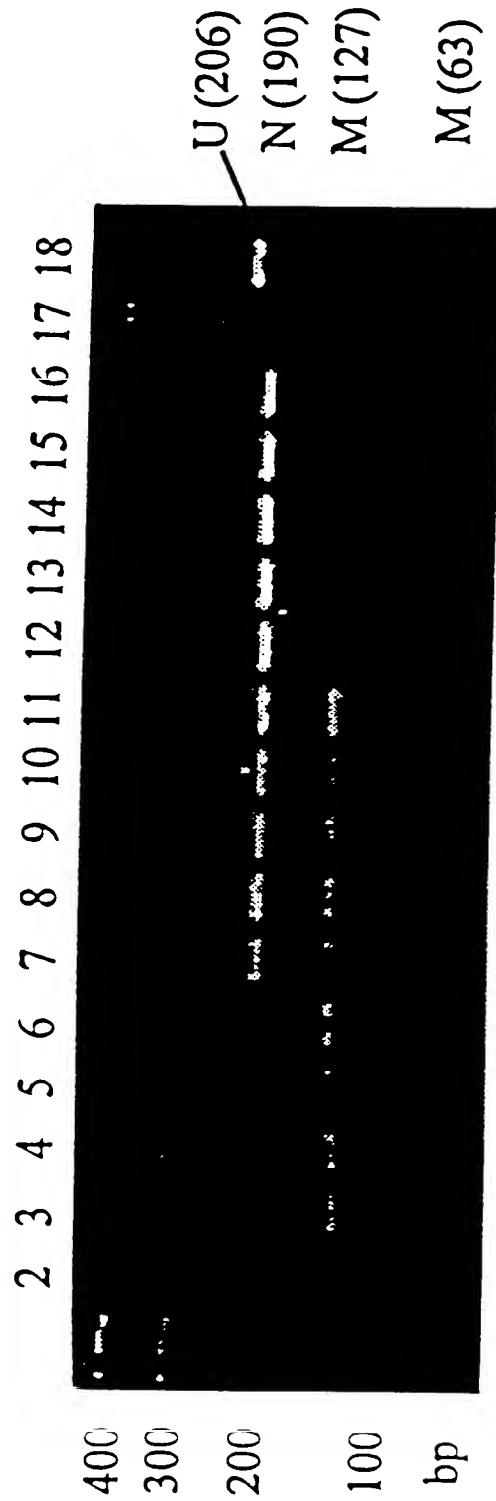
Figure 11

Figure 12